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Global gene expression analysis of cross-protected phenotype of pectobacterium atrosepticum

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Abstract

 The ability to adapt to adverse conditions permits many bacterial species to be virtually ubiquitous and survive in a variety of ecological niches. This ability is of particular importance for many plant pathogenic bacteria that should be able to exist, except for their host plants, in different environments e.g. soil, water, insect-vectors etc. Under some of these conditions, bacteria encounter absence of nutrients and persist, acquiring new properties related to resistance to a variety of stress factors (cross-protection). Although many studies describe the phenomenon of cross-protection and several regulatory components that induce the formation of resistant cells were elucidated, the global comparison of the physiology of cross-protected phenotype and growing cells has not been performed. In our study, we took advantage of RNA-Seq technology to gain better insights into the physiology of cross-protected cells on the example of a harmful phytopathogen, Pectobacterium atrosepticum (Pba) that causes crop losses all over the world. The success of this bacterium in plant colonization is related to both its virulence potential and ability to persist effectively under various stress conditions (including nutrient deprivation) retaining the ability to infect plants afterwards. In our previous studies, we showed Pba to be advanced in applying different adaptive strategies that led to manifestation of cell resistance to multiple stress factors. In the present study, we determined the period necessary for the formation of cross-protected Pba phenotype under starvation conditions, and compare the transcriptome profiles of non-adapted growing cells and of adapted cells after the cross-protective effect has reached the maximal level. The obtained data were verified using qRT-PCR. Genes that were expressed differentially (DEGs) in two cell types were classified into functional groups and categories using different approaches. As a result, we portrayed physiological features that distinguish cross-protected phenotype from the growing cells.

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